```
     FILE 'MEDLINE, BIOSIS' ENTERED AT 11:24:01 ON 09 NOV 1999
L1           238 S AMPLIFICATION METHODS
L2             0 S AMPLICATION BUFFERS
L3          5330 S DIMETHYLSULFOXIDE
L4             0 S L1 AND L3
L5         72313 S AMPLIFICATION
L6            23 S L3 AND L5
L7            13 S INTERCALATIVE DYE
L8             0 S L7 AND L5
L9        195811 S HYBRIDIZATION
L10            0 S L7 AND L9
L11            0 S AMPLIFICATION REAGENTS
L12           30 S PCR REAGENTS
L13          250 S MAGNESIUM ACETATE
L14            0 S L13 AND L5
L15            0 S L13 AND L12
L16            0 S CHLORIDE FREE RAGENTS
L17            0 S CHLORIDE FREE REAGENTS
L18       120374 S PCR
L19            0 S L18 AND L13
L20          575 S POTASSIUM ACETATE

=> l18 and l20
L18 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l18 and l20
L21            3 L18 AND L20

=> d l21 1-3 all
```

TRANSCRIPTIONAL REGULATION OF NEUROMODULIN GAP-43 IN MOUSE NEUROBLASTOMA CLONE N1E-115 AS EVALUATED BY THE RT-PCR METHOD.

AU ROBBINS M; MCKINNEY M

CS MAYO CLINIC JACKSONVILLE, JACKSONVILLE, FLA. 32224, USA.

SO MOL BRAIN RES, (1992) 13 (1-2), 83-92.
CODEN: MBREE4. ISSN: 0169-328X.

FS BA; OLD

LA English

AB The steady-state level of the neuromodulin transcript in the neuron-like N1E-115 cell line was measured with a method combining reverse transcription and the polymerase chain reaction (RT/PCR). Total RNA was isolated from N1E-115 cells and treated with DNAse to remove residual DNA; cDNA was synthesized from this RNA by priming with random hexamers. For PCR **amplification**, primers for neuromodulin were designed for regions of the coding sequence that were identical in mouse, rat, and human. In one approach (the 'ratio method'), variations in RNA yield and cDNA synthesis efficiency were controlled for by amplifying a reference (housekeeping) gene (glyceraldehyde phosphate dehydrogenase; GAPDH). To control for inter-experimental variations in PCR **amplification** efficiencies the data were analyzed on semi-logarithmic plots, with which the relative levels of starting templates could be determined by extrapolating the plots to cycle number zero (0). In another approach with RT/PCR (the 'spiking method'), the absolute level of N1E-115 neuromodulin cDNA was assessed by adding known amounts of cloned human neuromodulin template to the RT/PCR assay of N1E-115 nucleic acid and comparing the increased yield of product across cycles. When the spike was added at either the cDNA level (in the form of double-stranded DNA) or at the total RNA level (as sense RNA), the levels of N1E-115 calculated were virtually the same: 509 fg and 495 fg of coding region per ug total RNA in confluent N1E-115 cells, respectively. Treatment of N1E-115 cells with 2% **dimethylsulfoxide** for three days elevated neuromodulin mRNA levels by 5.6-fold. Conversely, treatment of N1E-115 cells with 100 nM phorbol myristate acetate for 24 h decreased the level of neuromodulin mRNA by 70%. Under carefully controlled conditions and within certain limits of precision, the RT/PCR method appears to be suitable for assessing the level of low abundance mRNA under various pharmacologically-induced conditions.

CC Cytology and Cytochemistry - Animal *02506
Genetics and Cytogenetics - Animal *03506
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Replication, Transcription, Translation *10300
Endocrine System - Neuroendocrinology *17020
Nervous System - Physiology and Biochemistry *20504
Neoplasms and Neoplastic Agents - Neoplastic Cell Lines 24005

BC Muridae 86375

IT Miscellaneous Descriptors
REVERSE TRANSCRIPTION POLYMERASE CHAIN REACTION

L6 ANSWER 22 OF 23 BIOSIS COPYRIGHT 1999 BIOSIS

AN 1986:115141 BIOSIS

DN BA81:25557

TI CHARACTERIZATION OF DIFFERENTIATION-INDUCER-RESISTANT HL-60 CELLS.

AU GALLAGHER R E; BILELLO P A; FERRARI A C; CHANG C-S; YEN R-W C; NICKOLS W A; MULY E C III

CS UNIV. MARYLAND CANCER CENT., ROOM 9-043 BRESSLER RES. BLG., 655 W.

BALTIMORE ST., BALTIMORE, MD. 21201, U.S.A.
SO LEUK RES, (1985) 9 (8), 967-986.

A touchdown PCR for the differentiation of equine herpesvirus type 1 (EHV-1) field strains from the modified live vaccine strain RacH.

AU Osterrieder, Nikolaus (1); Huebert, Peter H.; Brandmueller, Christine; Kaaden, Oskar-Rueger

CS (1) Inst. Med. Microbiol., Infectious Epidemic Diseases, Ludwig-Maximilians-Univ. Munich, Veterinaerstr. 13, 80539 Munich Germany

SO Journal of Virological Methods, (1994) Vol. 50, No. 1-3, pp. 129-136. ISSN: 0166-0934.

DT Article

LA English

AB More than 50 reference strains and field isolates of equine herpesvirus type 1 (EHV-1) were examined by a touchdown PCR. Primers for specific **amplification** of EHV-1 DNA were chosen from the terminal and internal repeat regions of the EHV-1 genome where the high-passaged live vaccine strain RacH displays symmetric 850 bp deletions. The positive strand and one negative strand primer were designed to encompass the deletions present in RacH, and the second negative strand primer was designed to hybridize within these deletions. Discrimination between field isolates and the vaccine strain was achieved by the generation of **amplification** products of different size: In all EHV-1 reference strains and field isolates, a 495 bp DNA fragment was amplified specifically, whereas a 310 bp fragment was amplified when DNA of the vaccine strain RacH was used as a template. PCR **amplification** was only obtained in the presence of 8-10% **dimethylsulfoxide** and when the primer annealing temperatures were decreased stepwise from 72 degree C to 60 degree C. Under these conditions as little as 100 fg template DNA, corresponding to about 100 genome equivalents, could be detected. The PCR assay allows fast and sensitive discrimination of the modified live vaccine strain RacH from field strains of EHV-1 since it is applicable to viral DNA extracted from organ samples and paraffin-embedded tissues. It may thus be helpful for examining the potential involvement of the RacH live vaccine strain in abortions of vaccinated mares.

CC Biochem

QR355.V61

L7 ANSWER 8 OF 13 BIOSIS COPYRIGHT 1999 BIOSIS
ACCESSION NUMBER: 1995:439767 BIOSIS
DOCUMENT NUMBER: PREV199598454067
TITLE: Homogeneous quantitative assay of hepatitis C virus RNA by polymerase chain reaction in the presence of a fluorescent intercalator.
AUTHOR(S): Ishiguro, Takahiko; Saitoh, Juichi; Yawata, Hideo; Yamagishi, Hiroaki; Iwasaki, Shuji; Mitoma, Yasutami
CORPORATE SOURCE: Scientific Instrument Div., Tosoh Corp., 2743-1 Hayakawa, Ayase-shi, Kanagawa 252 Japan
SOURCE: Analytical Biochemistry, (1995) Vol. 229, No. 2, pp. 207-213.
ISSN: 0003-2697.
DOCUMENT TYPE: Article
LANGUAGE: English
AB We have developed a homogeneous quantitative assay of DNA/RNA by performing PCR in the presence of an oxazole yellow derivative, a fluorescent DNA **intercalative dye**, and monitoring the fluorescence intensity of the PCR reaction mixture during PCR cycles. We have demonstrated the applicability of this assay by use it to quantify hepatitis C virus (HCV) RNA of serum samples from patients with chronic hepatitis C. This assay gave efficient and reproducible results in a clinically useful dynamic range below 10-6 copies of HCV RNA for interferon therapy.

CESSION NUMBER: 1998:182011 BIOSIS
DOCUMENT NUMBER: PREV199800182011
TITLE: Homogeneous assay of nucleic acid sequences by the fluorescence activation of DNA intercalator: Its application to HCV monitoring in IFN therapy.
AUTHOR(S): Ishiguro, Takahiko (1)
CORPORATE SOURCE: (1) TOSOH Corp., Tokyo Res. Lab., 2743-1 Hayakawa, Ayase 252 Japan
SOURCE: Japanese Journal of Electrophoresis, (Dec., 1997) Vol. 41, No. 6, pp. 293-300.
ISSN: 0031-9082.
DOCUMENT TYPE: Article
LANGUAGE: Japanese
SUMMARY LANGUAGE: Japanese; English

AB We demonstrated the application of IM-PCR, intercalation monitoring PCR, to quantify HCV RNA of serum samples from patients with chronic hepatitis C by performing PCR in the presence of oxazole yellow derivative, a fluorescent DNA **intercalative dye**, and monitoring the fluorescence intensity of the PCR reaction mixture in the course of PCR cycles. The assay gave the efficient and reproducible results in clinically useful dynamic range bellow 10-6 copies of HCV RNA for interferon therapy. We also reported here our novel fluorescent DNA probe, oxazole yellow (YO)-linked oligonucleotide complementary to a target DNA/RNA, which can enhance the fluorescence on hybridizing with a target nucleotide and its applicability to construct an assay of a sequence specific homogeneous detection of HCV RNA in clinical samples in conjunction with RT-PC

A novel, rapid in cell RNA amplification technique for the detection of low copy mRNA transcripts.

AUTHOR: Uhlmann V; Rolfs A; Mix E; Silva I; Hully J; Lu L; Lohman K; Howells D; Picton S; O'Leary J J

CORPORATE SOURCE: Department of Pathology, Cornell University Medical College, New York Hospital, NY 10021, USA.

SOURCE: MOLECULAR PATHOLOGY, (1998 Jun) 51 (3) 160-3.
Journal code: CNW. ISSN: 1366-8714.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199903

ENTRY WEEK: 19990301

AB Growing interest now focuses on improvements of in situ polymerase chain reaction (PCR) technology for the detection of DNA and RNA cellular sequences. In this study, reverse transcription PCR in situ hybridisation (RT PCR-ISH) was developed and used to determine gene expression of pyruvate dehydrogenase in a cell model system, using human peripheral blood lymphocytes (PBLs). The success of in cell RNA amplification depends on the type of cell/tissue fixation, cell permeabilisation, and the efficiency of reverse transcription and cDNA amplification. This paper presents new approaches to overcome the critical aspects of fixation, permeabilisation, and reverse transcription when performing in cell RNA amplification. A novel fixative, "Permeafix", possessing fixative and permeabilisation properties, was used for cell fixation procedures. "Permeafix" obviated the need for pre-amplification proteolysis, facilitating entry of **PCR reagents** to target sequences within the cell. In addition, a simple on step RNA in cell amplification protocol using recombinant Thermus thermophilus (rTth) DNA polymerase, which reverse transcribes mRNA efficiently to cDNA and then catalyses cDNA amplification, was used. The value of a semi-junctional primer system for in cell gene expression studies, without the need to perform DNase digestion, is demonst

Liquid chromatographic determination of oxytetracycline in swine tissues.

AUTHOR: Kawata S; Sato K; Nishikawa Y; Iwama K
CORPORATE SOURCE: Yokohama City Meat Inspection Office, Japan.
SOURCE: JOURNAL OF AOAC INTERNATIONAL, (1996 Nov-Dec) 79 (6) 1463-5.
Journal code: BKS. ISSN: 1060-3271.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199703
ENTRY WEEK: 19970303

AB A simple and rapid method was developed for determination of oxytetracycline (OTC) in swine muscle and kidney by liquid chromatography (LC). The method involved homogenization of sample in acetonitrile-1M imidazole buffer containing 10 mM disodium ethylenediaminetetraacetic acid (Na2.EDTA) and 50 mM **magnesium acetate** (15 + 85) with added hexane, centrifugation, removal of the hexane phase, and ultrafiltration of the supernatant. L-column ODS (150 x 4.6 mm) with a mobile phase of acetonitrile-1M imidazole buffer containing 50 mM **magnesium acetate** and 10 mM Na2.EDTA (10 + 90) was used for the LC separation. A fluorescence detector was used at an excitation wavelength of 380 nm and an emission wavelength of 520 nm. The calibration graph was linear from 1.25 to 200 ng OTC. Recoveries of OTC from swine tissue fortified at levels of 0.05-1.0 microgram/g ranged from 58.0 to 67.3%. The quantitation and detection limits were 0.05 and 0.04 microgram/g, respecti

1998012567 MEDLINE
DN 98012567
TI **PCR** amplification of crude microbial DNA extracted from soil.
AU Yeates C; Gillings M R; Davison A D; Altavilla N; Veal D A
CS Key Centre for Biodiversity and Bioresources, School of Biological Sciences, Macquarie University, Sydney, Australia..
cyeates@rna.bio.mq.edu.au
SO LETTERS IN APPLIED MICROBIOLOGY, (1997 Oct) 25 (4) 303-7.
Journal code: AL0. ISSN: 0266-8254.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; B
EM 199803
EW 19980302
AB A rapid, inexpensive, large-scale DNA extraction method involving minimal purification has been developed that is applicable to various soil types. DNA was extracted from 100 g of soil using direct lysis with glass beads and sodium dodecyl sulphate (SDS) followed by polyethylene glycol precipitation, **potassium acetate** precipitation, phenol extraction and isopropanol precipitation. The crude extract could be used in **PCR** directed at high-copy number (bacterial small subunit rRNA) and single-copy (fungal beta-tubulin) genes.
CT Check Tags: Support, Non-U.S. Gov't
Base Sequence
*DNA: GE, genetics
*DNA: IP, isolation & purification
DNA Primers: GE, genetics
DNA, Bacterial: GE, genetics
DNA, Bacterial: IP, isolation & purification
DNA, Fungal: GE, genetics
DNA, Fungal: IP, isolation & purification
DNA, Ribosomal: GE, genetics
DNA, Ribosomal: IP, isolation & purification
Evaluation Studies
Genes, Fungal
*Polymerase Chain Reaction: MT, methods
RNA, Bacterial: GE, genetics
RNA, Ribosomal, 16S: GE, genetics
*Soil Microbiology
Tubulin: GE, genetics
RN 9007-49-2 (DNA)
CN 0 (DNA Primers); 0 (DNA, Bacterial); 0 (DNA, Fungal); 0 (DNA, Ribosomal); 0 (RNA, Bacterial); 0 (RNA, Ribosomal, 16S); 0 (Tubulin)

L21 ANSWER 2 OF 3 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1997:510277 BIOSIS
DN PREV199799809480
TI **PCR** amplification of crude microbial DNA extracted from soil.
AU Yeates, C.; Gillings, M. R.; Davison, A. D.; Altavilla, N.; Veal, D. A.
CS Key Cent. Biodiversity and Bioresources, Macquarie Univ., NSW 2109 Australia
SO Letters in Applied Microbiology, (1997) Vol. 25, No. 4, pp. 303-307.
ISSN: 0266-8254.
DT Article
LA English
AB A rapid, inexpensive, large-scale DNA extraction method involving minimal purification has been developed that is applicable to various soil types. DNA was extracted from 100 g of soil using direct lysis with glass beads

QR-5731

and sodium dodecyl sulphate (SDS) followed by polyethylene glycol precipitation, **potassium acetate** precipitation, phenol extraction and isopropanol precipitation. The crude extract could be used in **PCR** directed at high-copy number (bacterial small subunit rRNA) and single-copy (fungal beta-tubulin) genes.

CC Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biophysics - Molecular Properties and Macromolecules *10506
Enzymes - Methods *10804
Soil Microbiology *40000

BC Microorganisms - Unspecified *01000

IT Major Concepts
Biochemistry and Molecular Biophysics; Enzymology (Biochemistry and Molecular Biophysics); Microbiology

IT Miscellaneous Descriptors
ANALYTICAL METHOD; BIOCHEMISTRY AND BIOPHYSICS; MICROBIAL DNA; POLYMERASE CHAIN REACTION; SOIL EXTRACTION; SOIL SCIENCE

ORGN Organism Name
microorganism (Microorganisms - Unspecified); microorganisms (Microorganisms - Unspecified)

ORGN Organism Superterms
microorganisms

L21 ANSWER 3 OF 3 BIOSIS COPYRIGHT 1999 BIOSIS

AN 1995:531925 BIOSIS

DN PREV199598546225

TI An improved method for **PCR**-based detection of nuclear polyhedrosis virus in Bombyx mori.

AU Noguchi, Youko (1); Kobayashi, Masahiko; Shimada, Toru

CS (1) Saitama-Ken Sericultural Experiment Stn., Ishihara, Kumagaya, Saitama 360 Japan

SO Journal of Sericultural Science of Japan, (1995) Vol. 64, No. 4, pp. 352-359.
ISSN: 0037-2455.

DT Article

LA Japanese

SL Japanese; English

AB We have already established a diagnostic technique based on the polymerase chain reaction to detect nuclear polyhedrosis virus in a silkworm population using samples containing the wastes and feces as well as larval bodies. In the present study, we utilized **potassium acetate** Precipitation instead of phenol/chloroform treatment at the deproteinization step of DNA extraction, thus avoiding danger of applying a large amount of organic solvents. Also HCl treatment of DNA followed by ethanol precipitation was found to be effective to increase the diagnostic sensitivity. By using this improved method, we could detect a single polyhedrosis-infected larva in a 0.5, 1 and 3 kg sample for the 1st, 2nd and 3rd instar, respectively.

CC Biochemical Methods - General *10050
Biochemical Studies - General 10060
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biophysics - General Biophysical Techniques *10504
Enzymes - Methods *10804
Pathology, General and Miscellaneous - Diagnostic *12504
Virology - Animal Host Viruses *33506
Medical and Clinical Microbiology - Virology *36006
Veterinary Science - Pathology *38004
Veterinary Science - Microbiology *38006
Economic Entomology - Sericulture *60020
Invertebrata, Comparative and Experimental Morphology, Physiology and Pathology - Insecta - Physiology *64076

BC Animal Viruses - General 02600
Lepidoptera *75330

IT Major Concepts
Economic Entomology; Enzymology (Biochemistry and Molecular Biophysics); Infection; Methods and Techniques; Microbiology; Pathology; Physiology; Veterinary Medicine (Medical Sciences)
IT Industry
biotechnology industry; clothing industry
IT Miscellaneous Descriptors
DIAGNOSTIC METHOD; POLYMERASE CHAIN REACTION; PRODUCTIVITY
ORGN Super Taxa
Animal Viruses - General: Viruses; Insecta - Unspecified: Insecta, Arthropoda, Invertebrata, Animalia; Lepidoptera: Insecta, Arthropoda, Invertebrata, Animalia
ORGN Organism Name
animal viruses (Animal Viruses - General); insect (Insecta - Unspecified); microorganism (Microorganisms - Unspecified); Bombyx mori
(Lepidoptera)
O

WEST

Freeform Search

Database: US Patents Full-Text Database

Term: l8 and l4 or l8 and l5

Display 10 **Documents in Display Format:** TI

Generate: ○ **Hit List** ◉ **Hit Count** ○ **Image**

Search

Main Menu | Show S Numbers | Edit S Numbers

Search History

DB Name	Query	Hit Count	Set Name
USPT	5976832[uref]	0	L10
USPT	l8 and l4 or l8 and l5	66	L9
USPT	PCR adj buffer	797	L8
USPT	l6 and l4	22	L7
USPT	l1 and l3	231	L6
USPT	magnesium acetate	2970	L5
USPT	potassium acetate	7270	L4
USPT	Amplification adj reaction	1307	L3
USPT	acetate	234929	L2
USPT	chloride and inhibition	43043	L1

WEST

Freeform Search

Database: US Patents Full-Text Database

Term:

Display 10 **Documents in Display Format:** TI

Generate: ○ **Hit List** ◉ **Hit Count** ○ **Image**

Search

Main Menu | Show S Numbers | Edit S Numbers

Search History

DB Name	Query	Hit Count	Set Name
ALL	l19 and l17	1	L22
ALL	l19 and l17	1	L21
ALL	l19 and l16	2	L20
ALL	l14 and l15	80	L19
ALL	florescent signal	5	L18
ALL	l2 and l10	104	L17
ALL	l2 and l9	69	L16
ALL	l2 and l8	482	L15
ALL	l2 and l7	398	L14
ALL	l7 and l8 and l9 and l10	0	L13
ALL	l2 and l7 and l8 and l9 and l10	0	L12
ALL	phage SP6 polymerase	2	L11
ALL	dimethyl sulfoxide	26884	L10
ALL	RNaseH	309	L9
ALL	ribozyme or DNAzyme	1971	L8
ALL	detectable label	2259	L7
ALL	l2 and l3 and l4	13	L6
ALL	DNA-dependent DNA polymerase or DNA-dependent RNA polymerase	307	L5
ALL	RNA-dependent DNA polymerase	278	L4
ALL	single stranded oligonucleotide	647	L3
ALL	target nucleic acid	3129	L2
ALL	method of assay of target nucleic acid	0	L1

WEST

Main Menu | Search Form | Posting Counts | Show S Numbers | Edit S Numbers

Search Results -

Term	Documents
RNA-DEPENDENT	528
DNA	78818
POLYMERASE	19566
RNA-DEPENDENT ADJ DNA ADJ POLYMERASE	278

Database: All Databases (USPT + EPAB + JPAB + DWPI + TDBD)

Refine Search: RNA-dependent DNA polymerase

Search History

DB Name	Query	Hit Count	Set Name
ALL	RNA-dependent DNA polymerase	278	L4
ALL	single stranded oligonucleotide	647	L3
ALL	target nucleic acid	3129	L2
ALL	method of assay of target nucleic acid	0	L1

13 OF 53 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:363551 CAPLUS
DOCUMENT NUMBER: 125:29120
TITLE: Finderon analogs of ribozymes for endonucleolytic **cleavage** of **single-stranded RNA**
INVENTOR(S): Goodchild, John; Leonard, Thomas E.
PATENT ASSIGNEE(S): Hybridon, Inc., USA
SOURCE: PCT Int. Appl., 63 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9610080	A1	19960404	WO 1995-US12173	19950925
W: AM, AT, AU, BB, BG, BR, BY, CA, CN, CZ, DE, DK, EE, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TT, UA, UG				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5700923	A	19971223	US 1994-315287	19940929
US 5627055	A	19970506	US 1995-475867	19950607
US 5646021	A	19970708	US 1995-477883	19950607
US 5679554	A	19971021	US 1995-472427	19950607
CA 2200845	AA	19960404	CA 1995-2200845	19950925
AU 9536399	A1	19960419	AU 1995-36399	19950925
EP 783570	A1	19970716	EP 1995-933923	19950925
R: AT, BE, CH, DE, FR, LI				

PRIORITY APPLN. INFO.: US 1994-315287 19940929
WO 1995-US12173 19950925

AB A finderon has the ability to endonucleolytically **cleave** a sequence of 3'-to-5'-linked ribonucleotides. The finderon includes a rigid linker comprising at least one non-nucleotidic unit, flanked by first and second flanking regions of .gtoreq.4 contiguous, covalently-linked nucleotides. At least a portion of each flanking region is complementary to a target region on a substrate RNA mol. Thus, a finderon is a ribozyme with the entire catalytic region replaced by non-nucleotidic units. The non-nucleotidic linker may comprise cyclohexane diols, steroids, lupene diols, or isosorbides. Several finderons were synthesized contg. trans-1-O-(4,4'-dimethoxytrityl)-2-O-[.beta.-cyanoethoxy-(N,N-diisopropylamino)]phosphino-1,2-cyclohexanediol units flanked by ribo/deoxyribooligonucleotide regions **specific** for a **target** RNA mol. Facilitator oligonucleotides may be selected to bind to a sequence contiguous with the substrate sequence to which a flanking region binds at the 5' or the 3'-side of the finderon. Also disclosed are methods of prepg. and using a finderon, and kits including a finderon. Finderons are useful as **RNA-specific** restriction endonucleases for the manipulation of RNA mols.

DUPLICATE 7

L8 ANSWER 14 OF 53 MEDLINE
ACCESSION NUMBER: 96433149 MEDLINE
DOCUMENT NUMBER: 96433149 PubMed ID: 8836177
TITLE: Towards artificial ribonucleases: the sequence-